

Figure 1

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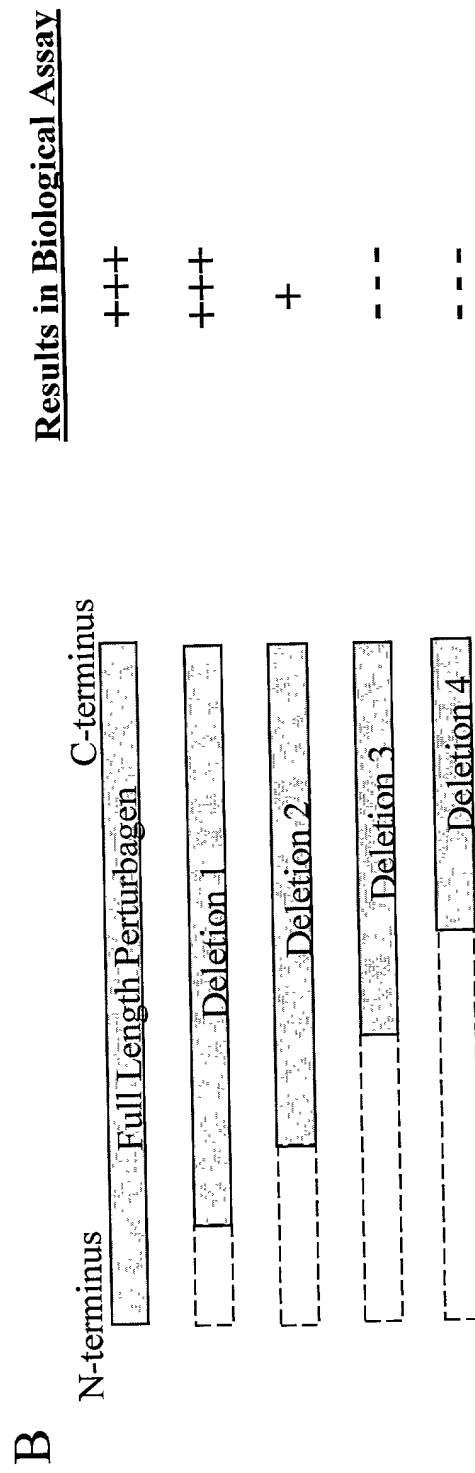
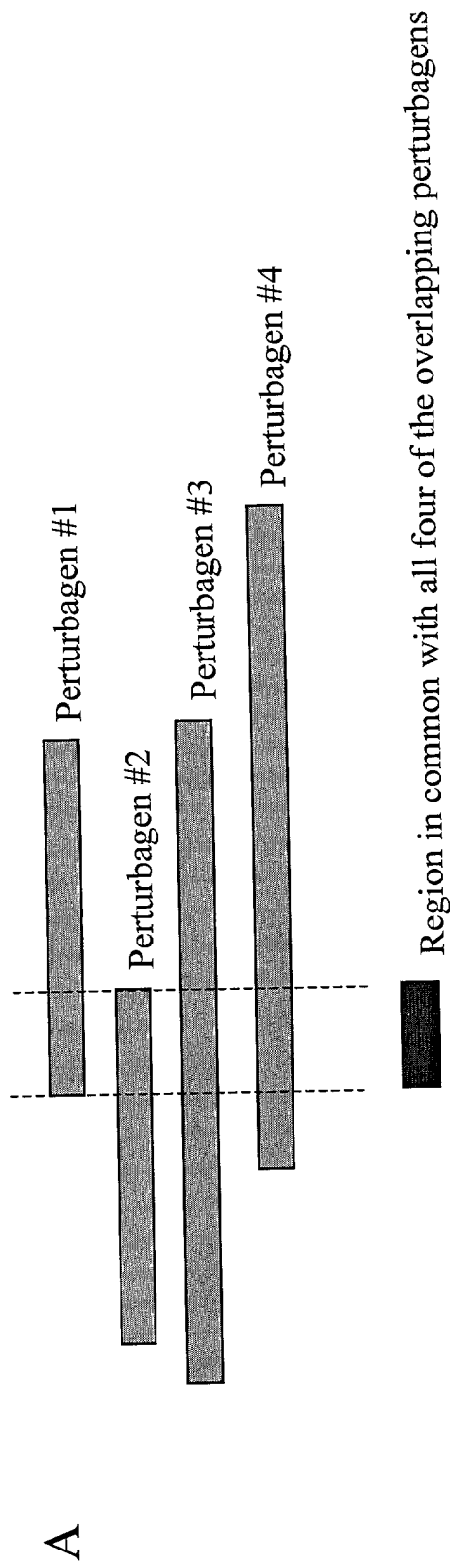


Figure 2

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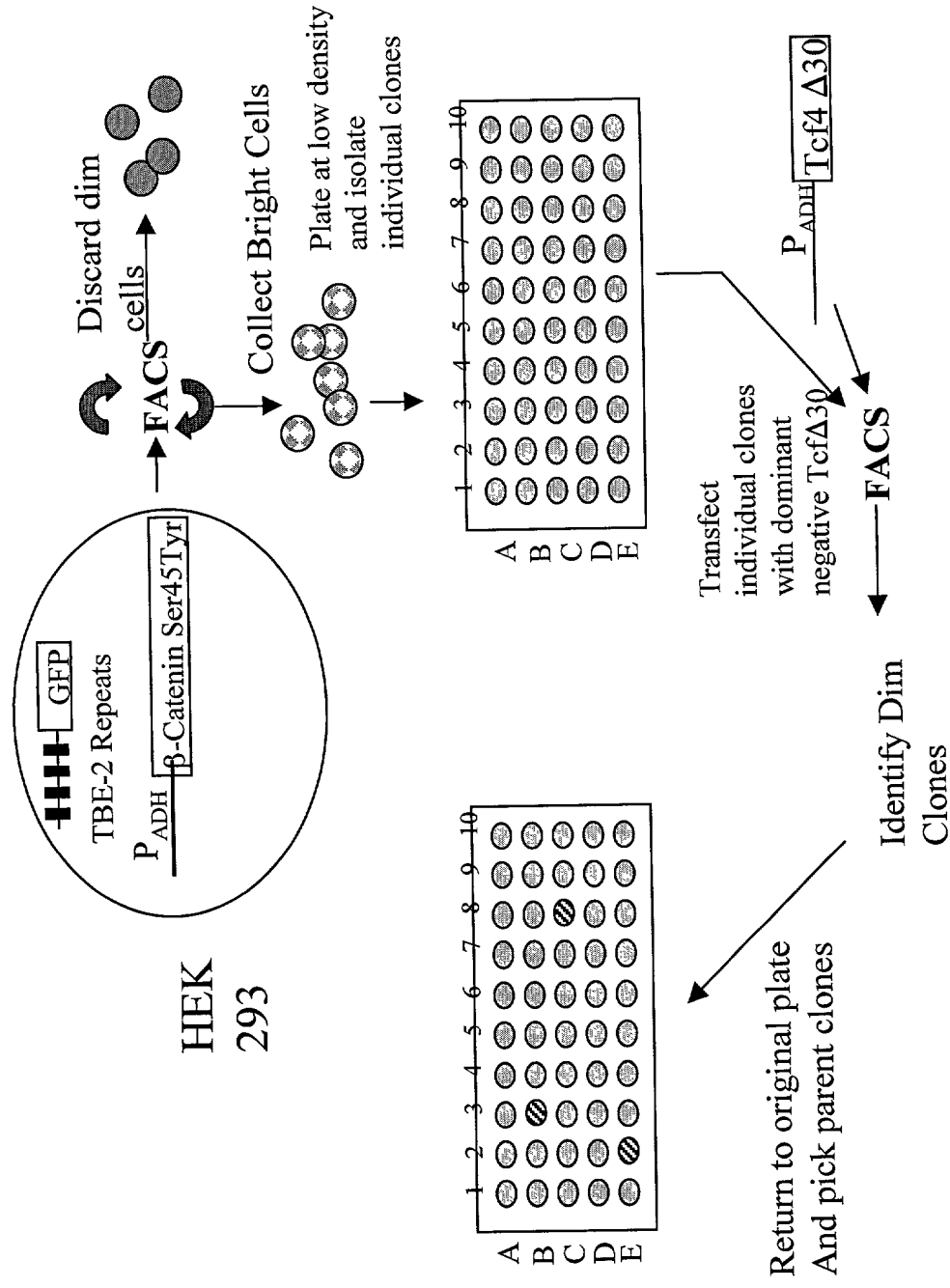


Figure 3

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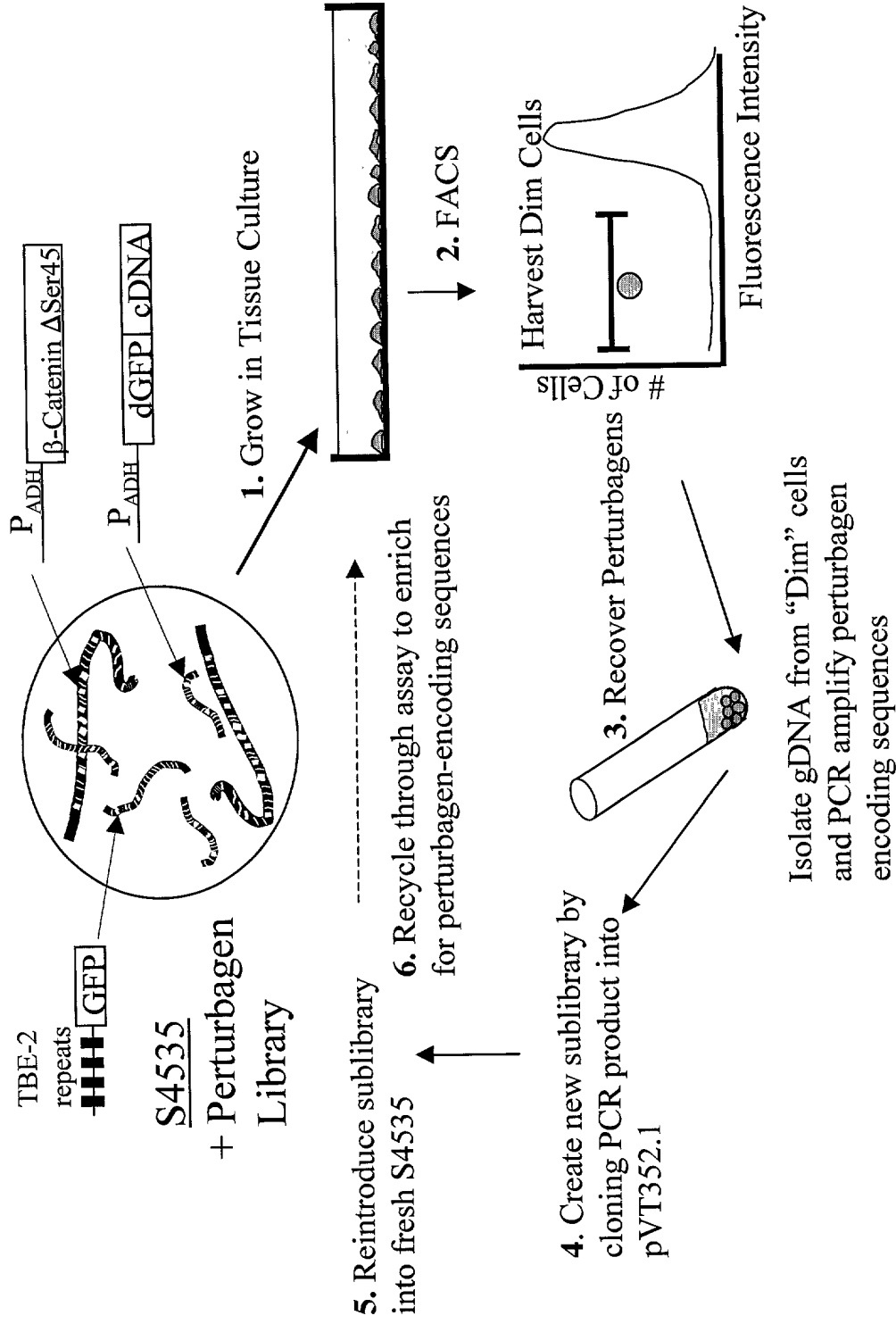


Figure 4

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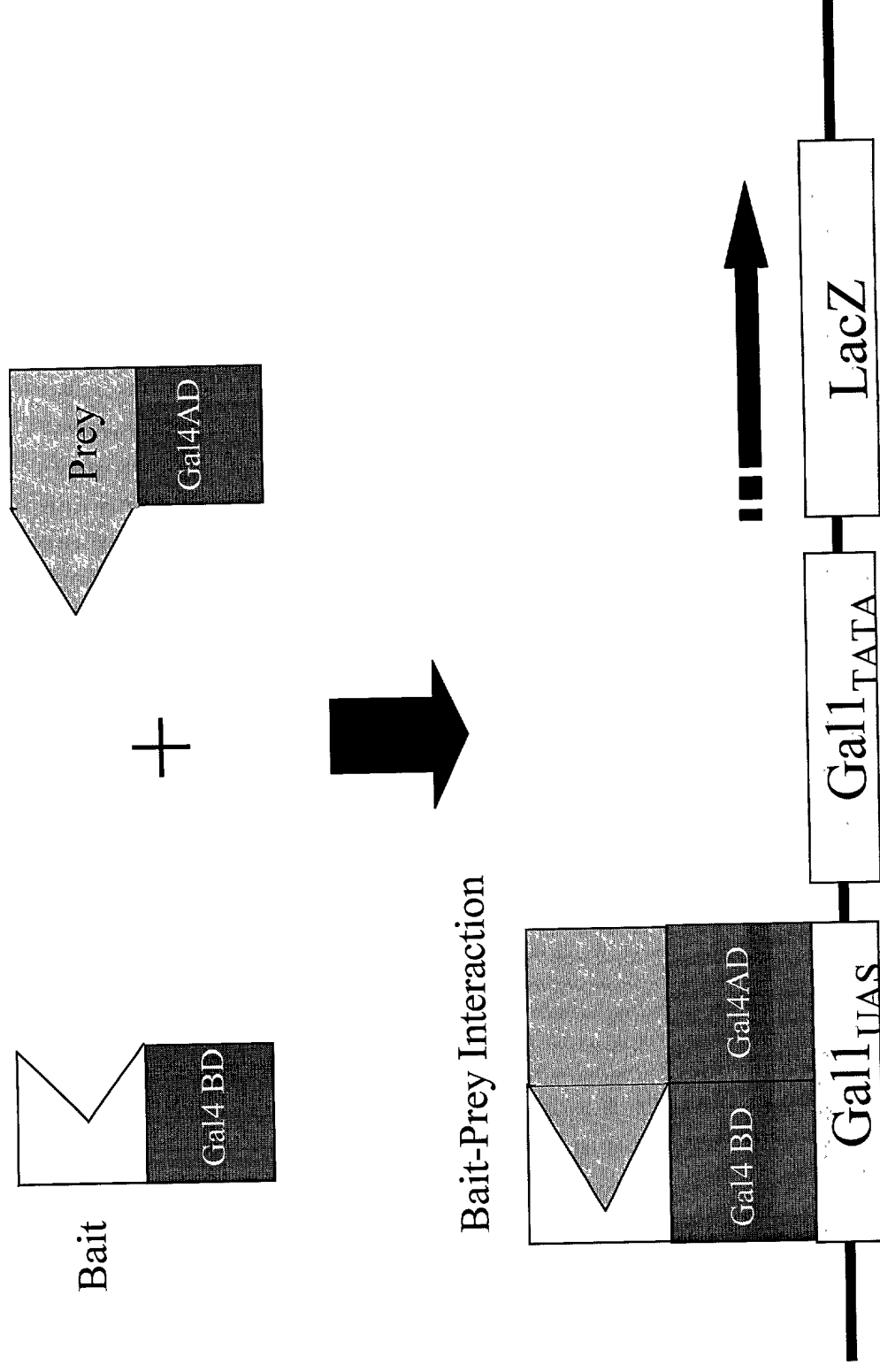


Figure 5

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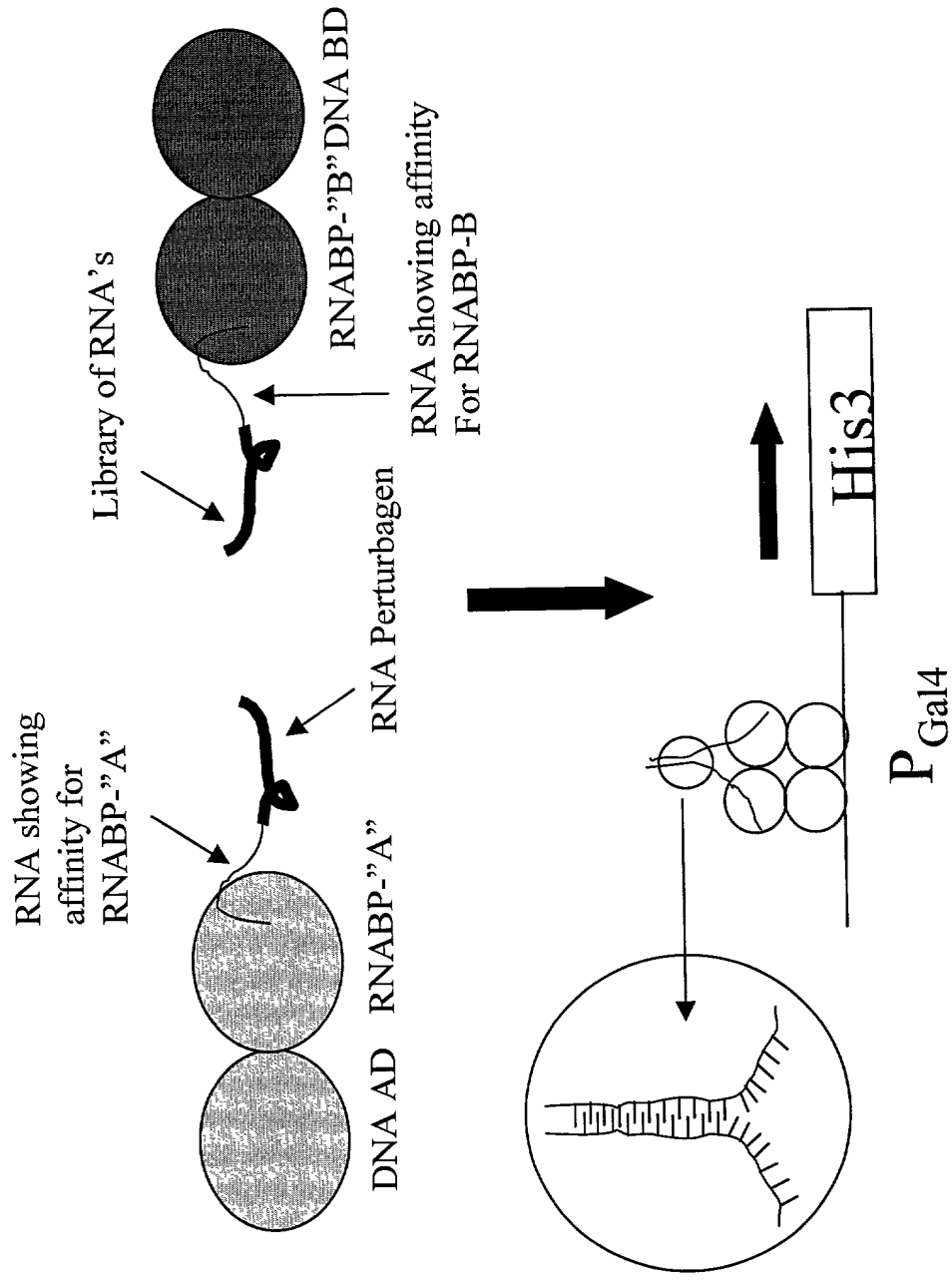


Figure 6

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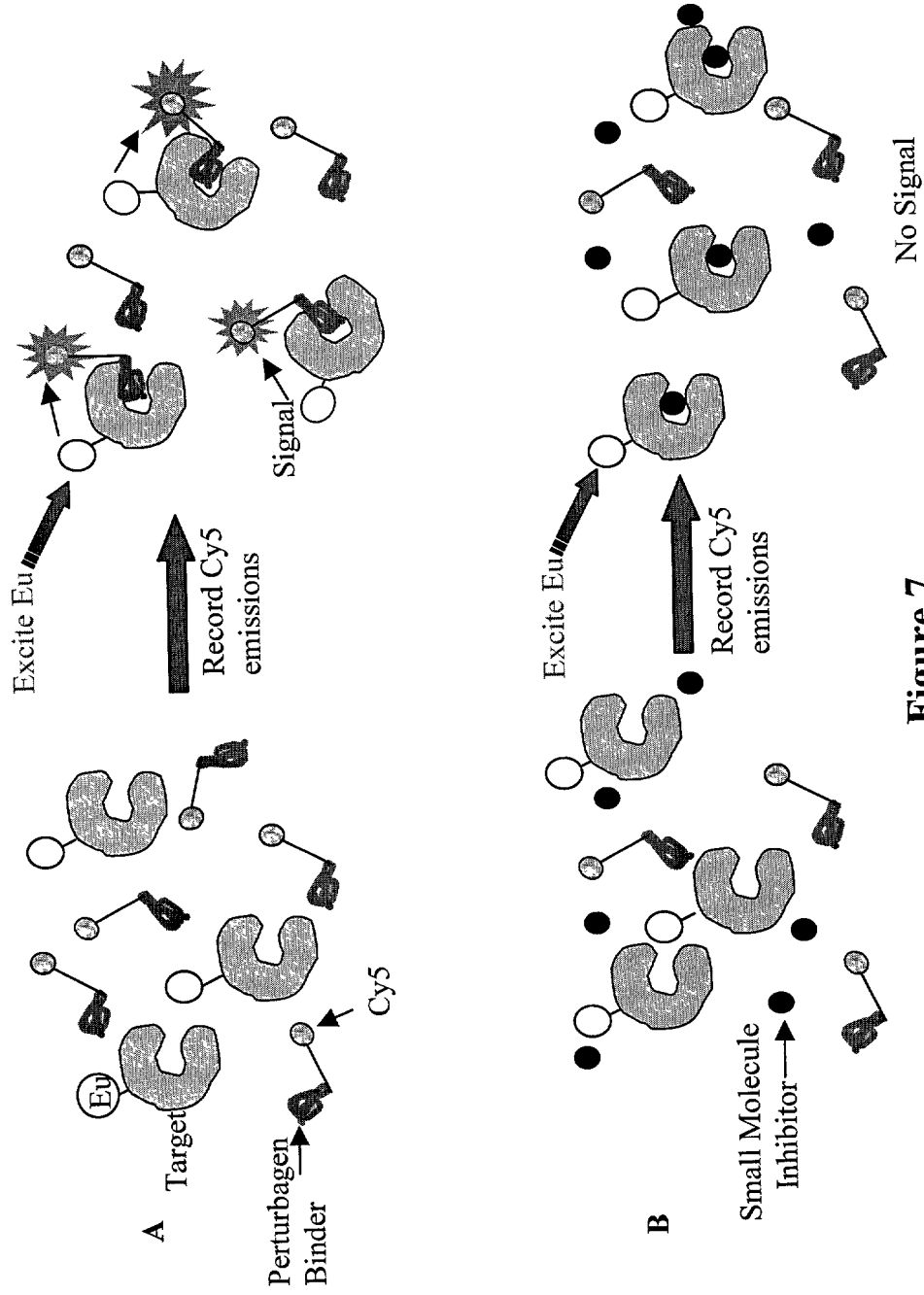


Figure 7

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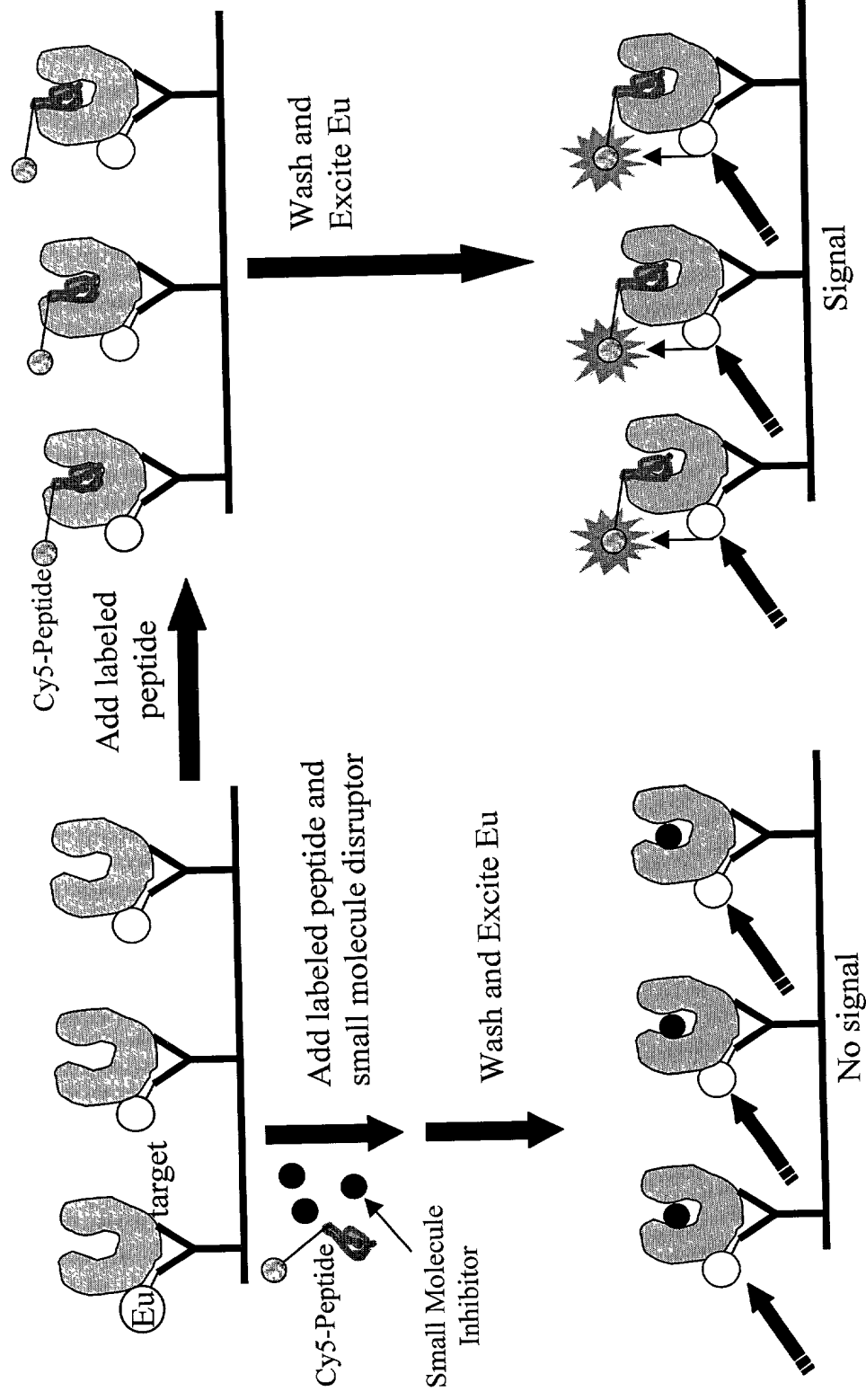


Figure 8

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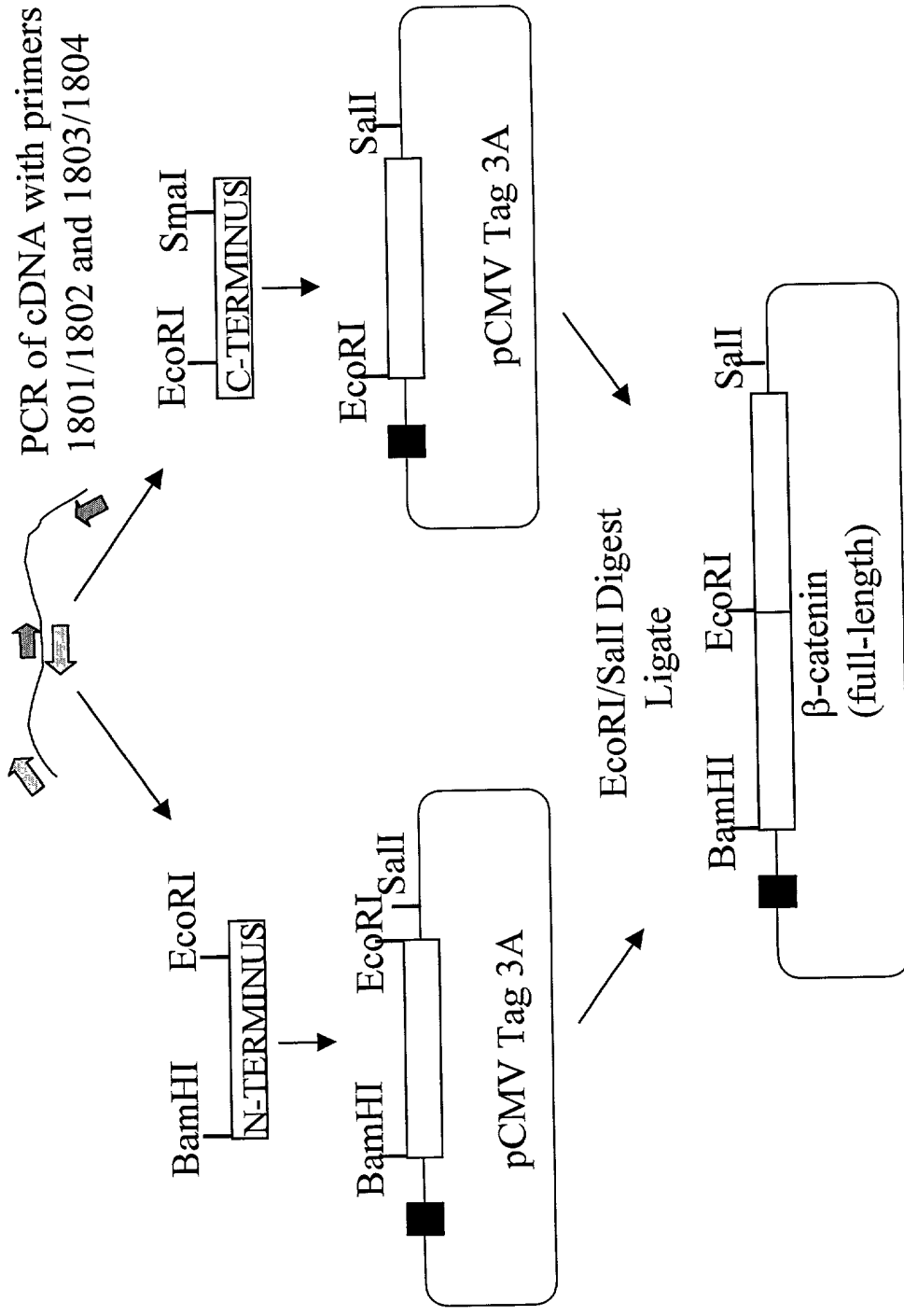


Figure 9

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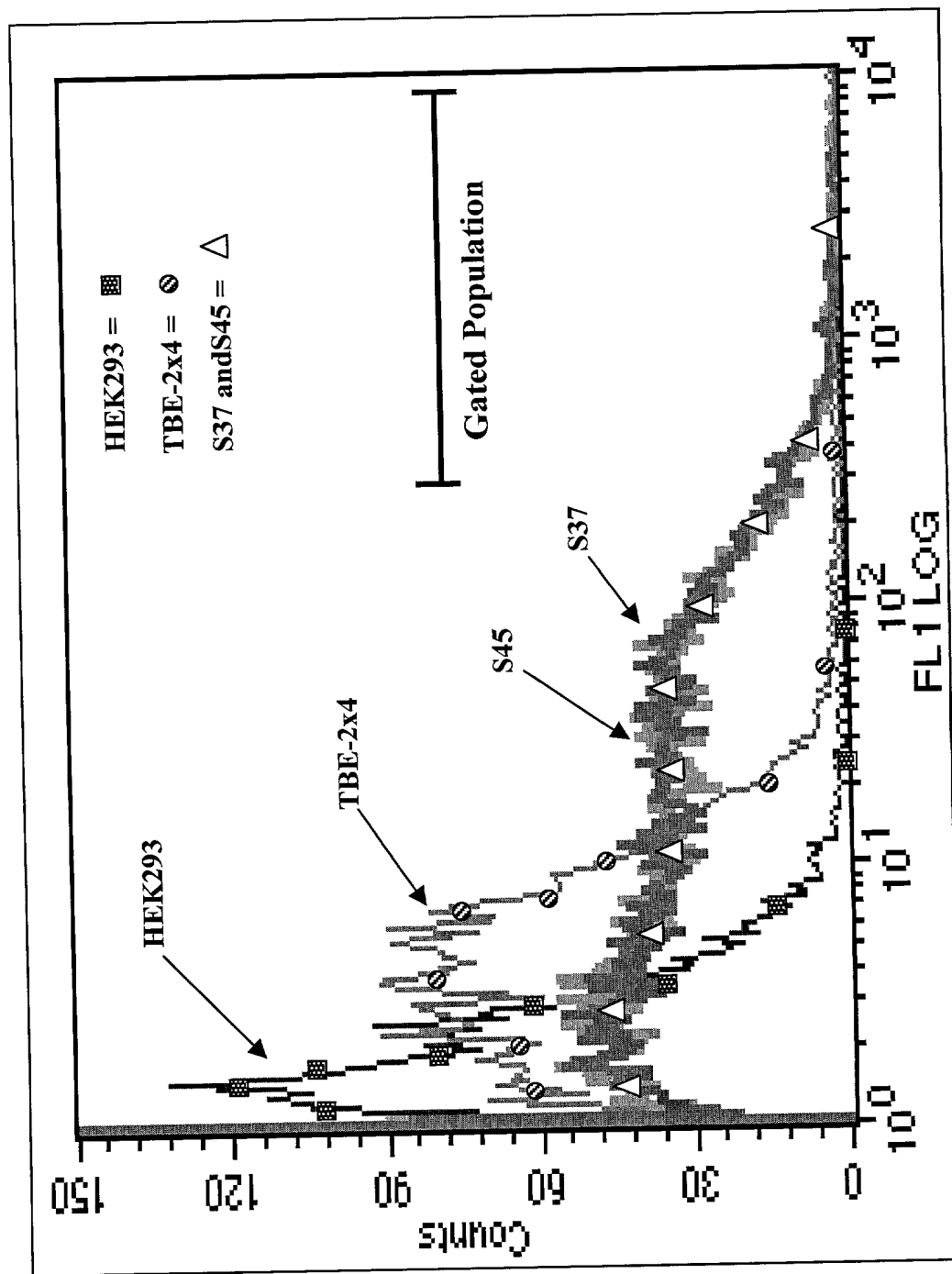


Figure 11

TC9TTC2T606600

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(3):SY000006 LMD FL1 LOG singles

TBE2EGFP

X-Mean: 1.2

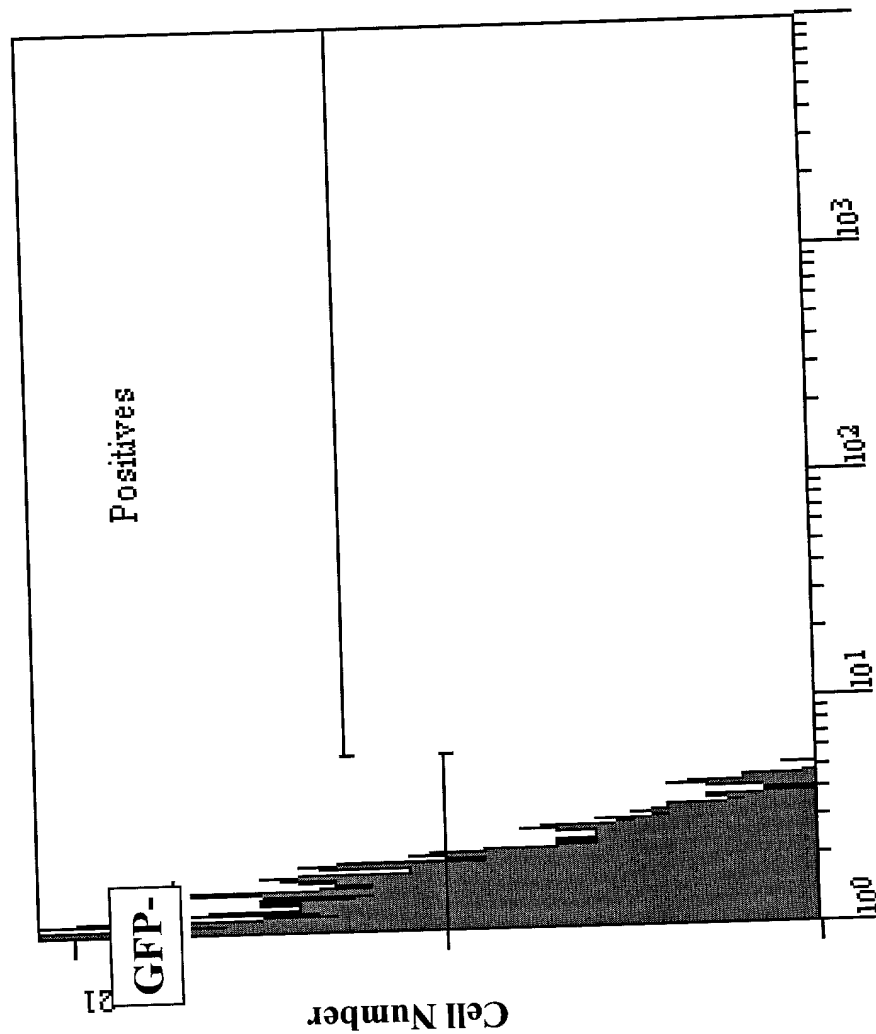


Figure 12A

FL1 LOG

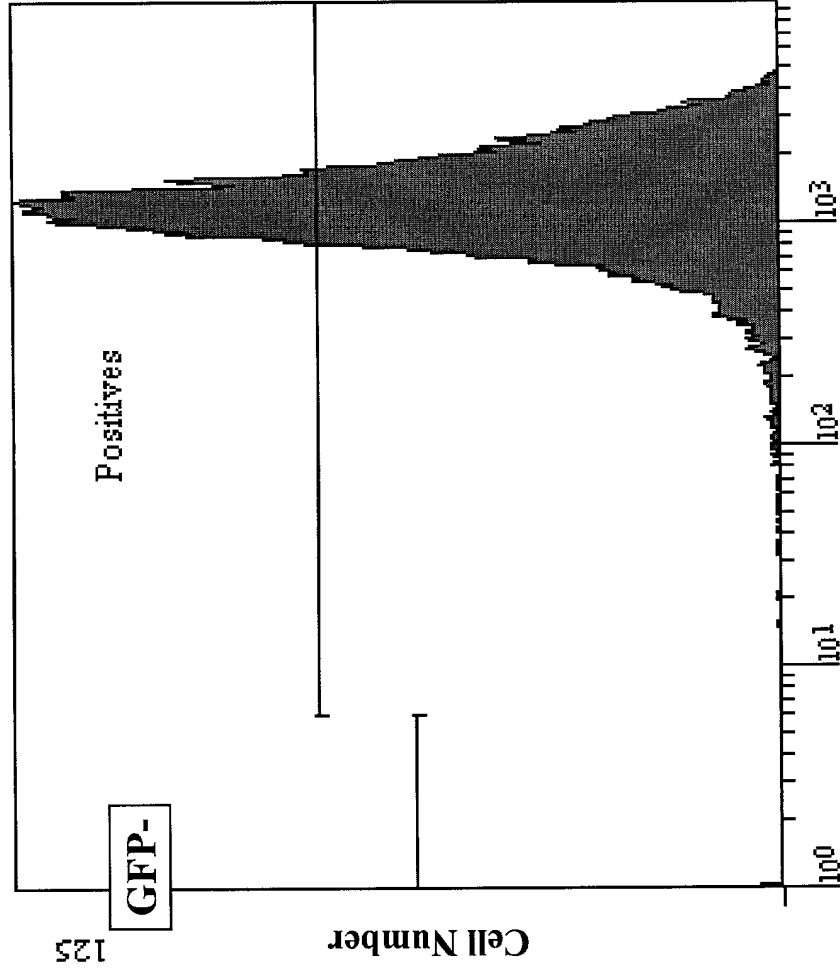
40947-260000

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(2)SY000027 LMD FL1 LOG singles

S45-35

X-Mean:1304.1



FL1 LOG

Figure 12B

Cell number

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(3):SY0000028.LMD FL1 LOG Singles

+dGFPΔTcf4DI

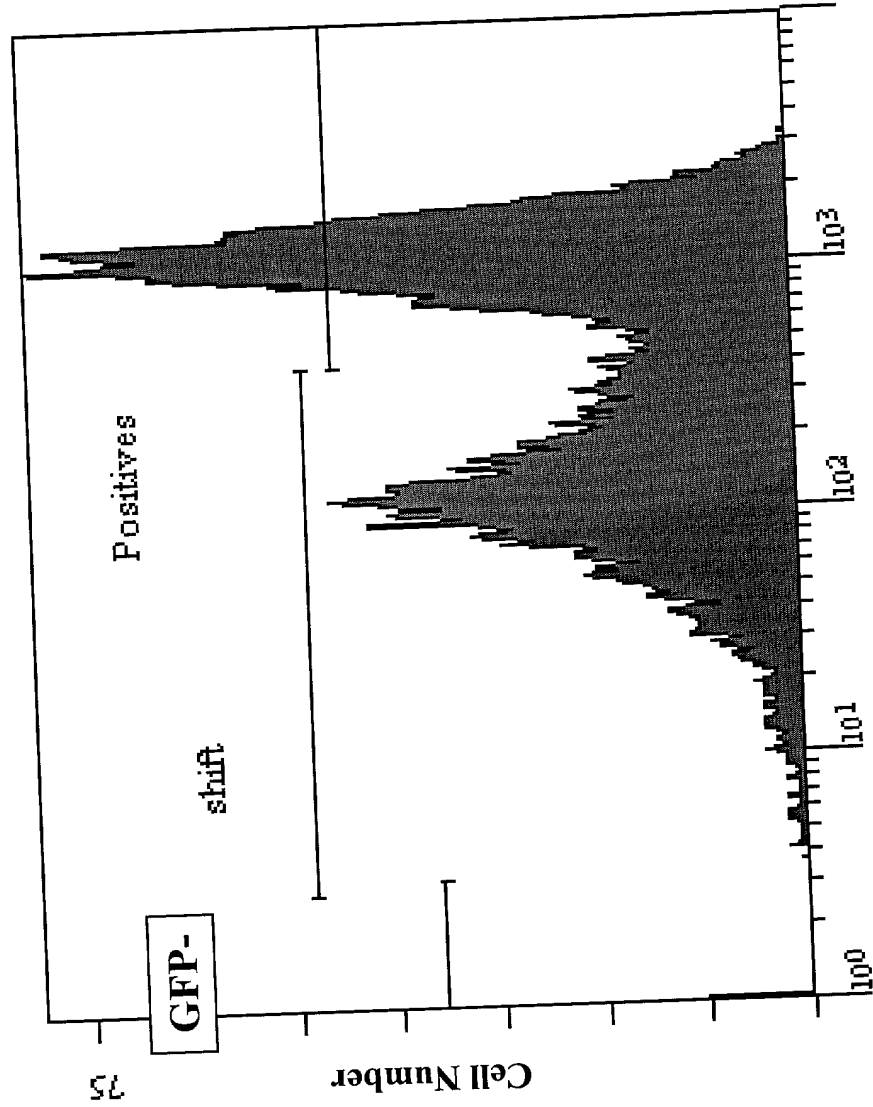


Figure 12C

FL1 LOG

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CADHERIN V PERTURBAGEN

DNA SEQUENCE

5' TTCCCTCTATGCGCAGGTGCAGAAAGCCACCGAGGCCACGCGCCTGGGGCACAC
GGAGGGCCCGGGAGATGGCAGCCATGATCGAGGTGAAGAACGAGCGCGGA
CCACGACGGCAGGCCCCCTACGACACGCTGCACATCTACGGCTACGAGGG
CTCCAAGTCCATAGCCAAGTCCCTCAGCTCCCTGGGCACCGACTCATCCGACTCT
GACATGGATTACGACTTCCTTAACGACTGGGACCCAGGTTTAAGATGCTGGCTG
AGCTGTACGGCTCGGACCCCGGAAGAGGCCA

PEPTIDE SEQUENCE

PYGSRNVSKIKCCCNGLAFSLMHIEYALLAIMESMFISLGEQTSLSLCTFQGPQGVL
CPEPWVPSKPRGVLCHGLRFVWQGSLLPPFGTELA VPK

Figure 13

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CADHERIN VI PERTURBAGEN

DNA SEQUENCE

GCGAAAAAAA	GAGCCTTTGA	TCATTTCCAA	AGAGGACATC	AGAGATAACA
TTGTCAGTTA	CAACGACGAA	GGTGGTGGAG	AGGAGGACAC	CCAGGCTTTT
GATATCGGCA	CCCTGAGGAA	TCCCTGAAGCC	ATAGAGGACA	ACAAATTACG
AAGGGACATT	GTGCCCCGAAG	CCCTTTTCCT	ACCCCGACGG	ACTCCAACAG
CTCGCGACAA	CACCGATGTC	AGAGATTTC	TTAACCCTTGG	GTTAAAGGAA
AATGACACGG	ACCCCACTGC	CCCGCCATAC	GACTCCTTGG	CCACTTACGC
CTATGAAGGC	ACTGGCTCCG	TGGCGGATTC	CCTGAGCTCG	CTGGAGTCAG
TGACCAACGA	TGCAGATCAA	GACTATGATT	ACCTTAGTGA	CTGGGGACCT
CGATTCAAAA	AGCTTGCAGA	TATGTATGGA	GGAGTGGACA	GTGACAAAGA
CTCCTAATCT	GTGCGCTTTT	TCATTTTCCA	ATACGACACT	GAAATATGTG
AAGTGGNTAT	TTTCTTTATA	TTTTACCCAC	TACNNGGAAA	

PEPTIDE SEQUENCE

PRKKEPLIISXXDIXDNIVSYNDEGGGEEDTQAFDIGTLRNPEAIEDNKLRRDIV
PEALFLPR

Figure 14

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CADHERIN XI

DNA SEQUENCE

TAGACCTGGGCTCCGGCCAGCGCCCAACAGCGTGGATGTCGATGACTTCATCAA
CACGAGAAATACAGGAGGCAGACAAATGACCCACGGCTCCTTATGACTCCAT
TCAAATCTACGGTTATAAGGCAGGGCTCAGTGGCCGGTCCCTGAGCTCCCT
AGAGTCGGCCACCACAGATTTCAGACTTGGACTATGATTATCTACAGAACTGGGG
ACCTCGTTTTAAGAAACTAGCAGATTGTATGTTCCAAAGACACTTTTGATGAC
GATTCTTAACAATAACGATACAAATTTGGCCTTAAGAACTGTGTCTGGCGTTCTC
AAGAACTAGAGATGTGTAAACAGGTATTTTTTAAATCAAGGAAAGGCTCAT
TTAAACAGGCAAAGTTTTACAGAGAGGATACATTTAATAAACTGCGAGGACA
TCAAAGGGTAAA

PEPTIDE SEQUENCE

PRPGLRPAPNSVDVDDFINTRIQEADNDPTAPPYDSIQIYGYEGRGSVAGSLSSLES
ATTDSLDLDYQLQNWGPRFKKLADLYGSKDTFDDDS

Figure 15

10947-20000

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singles FL1 LOG

Cadherin V

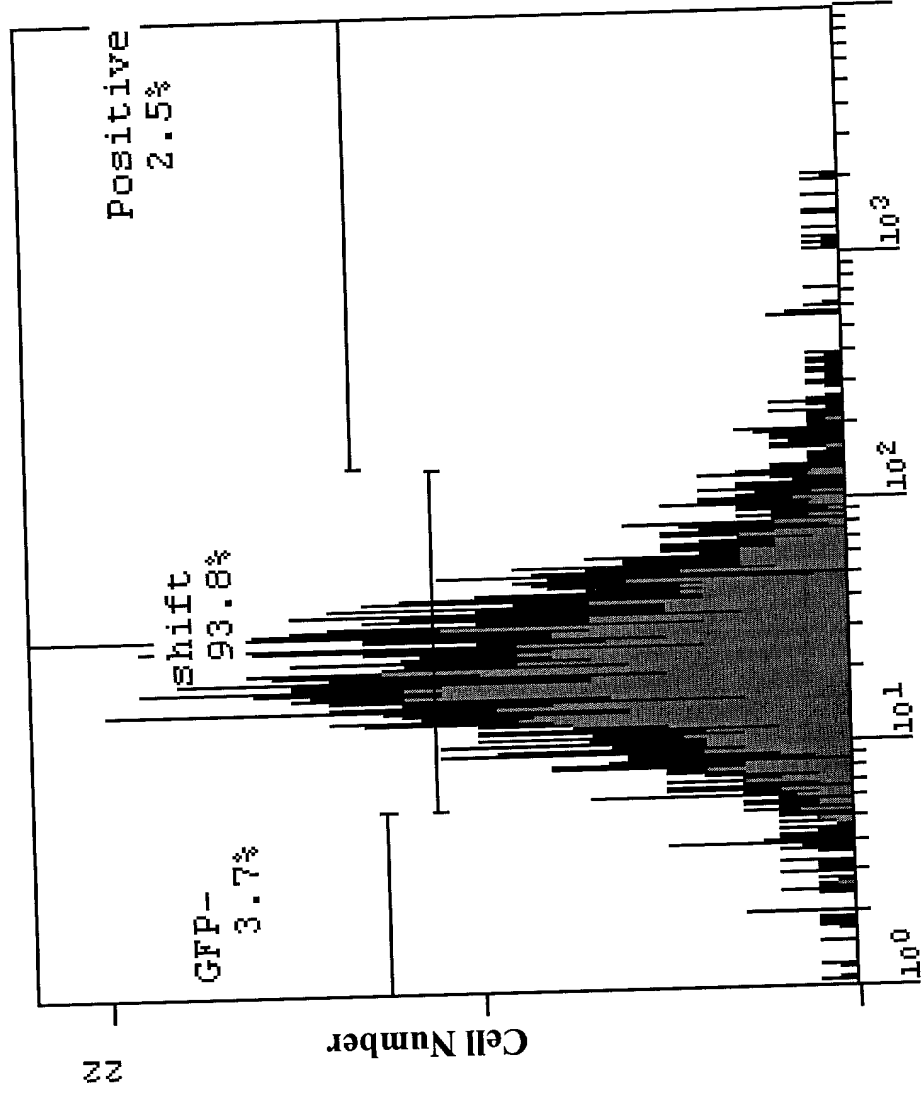


Figure 16

FL1 LOG

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Dead Cell Number

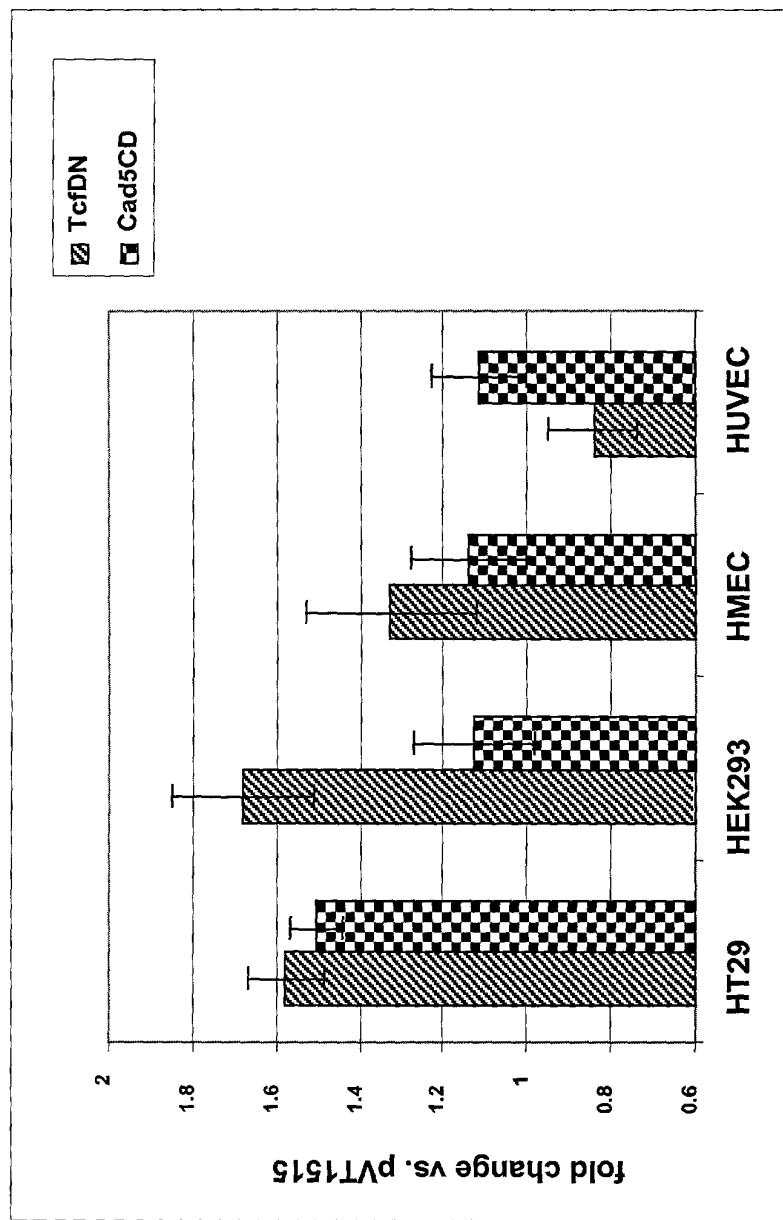


Figure 17

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Total Cell Number

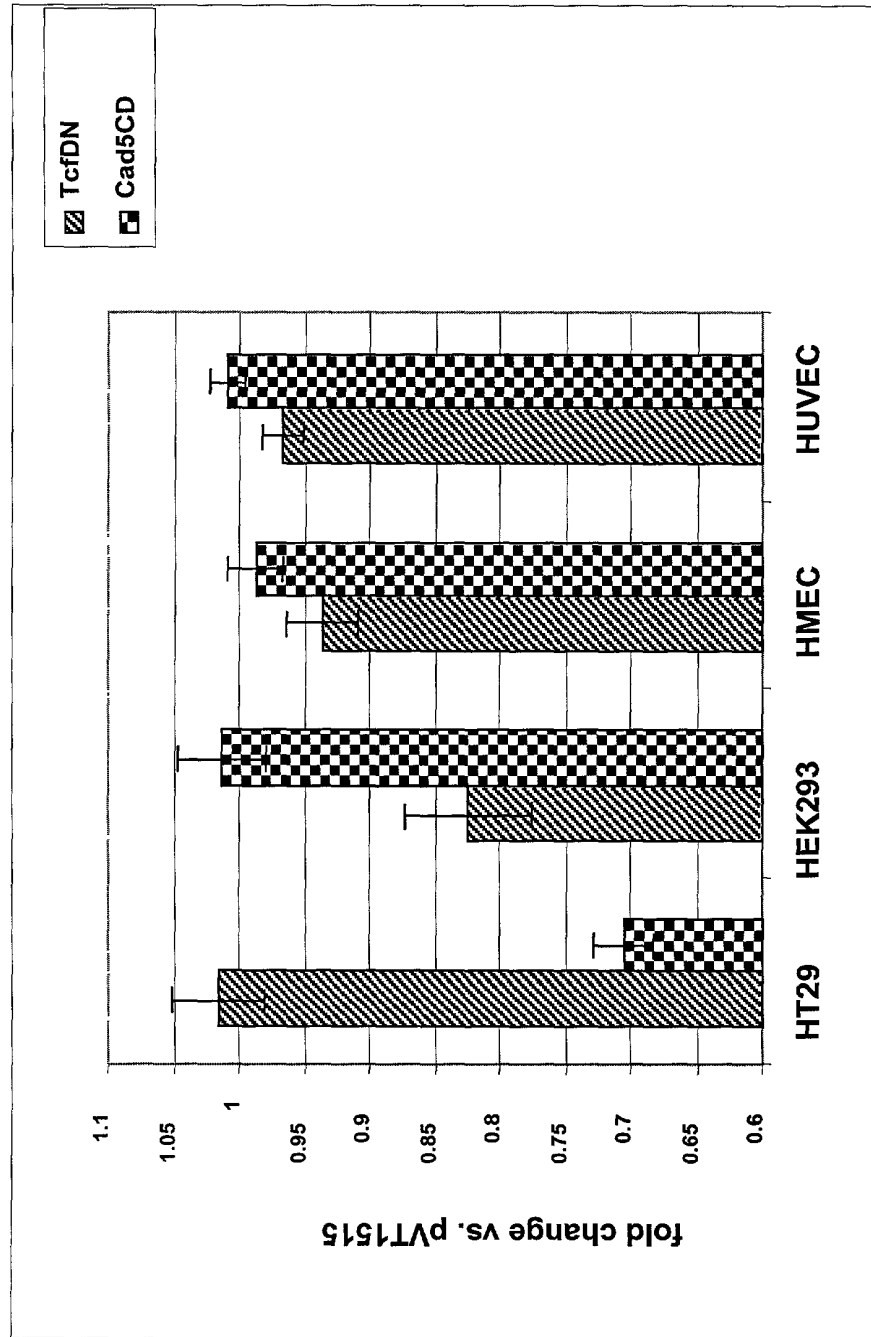


Figure 18

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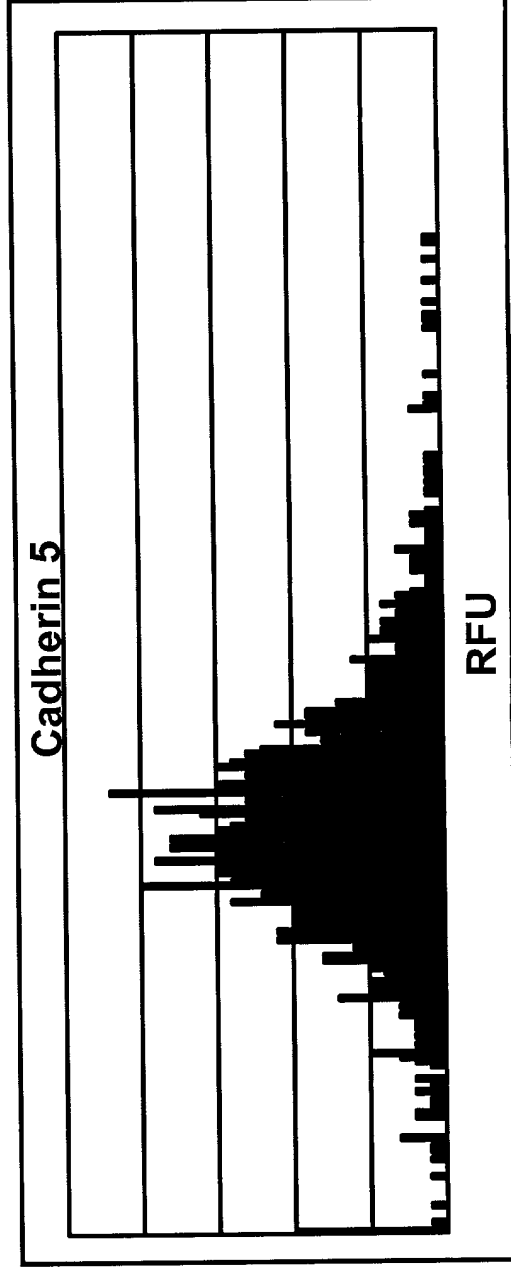
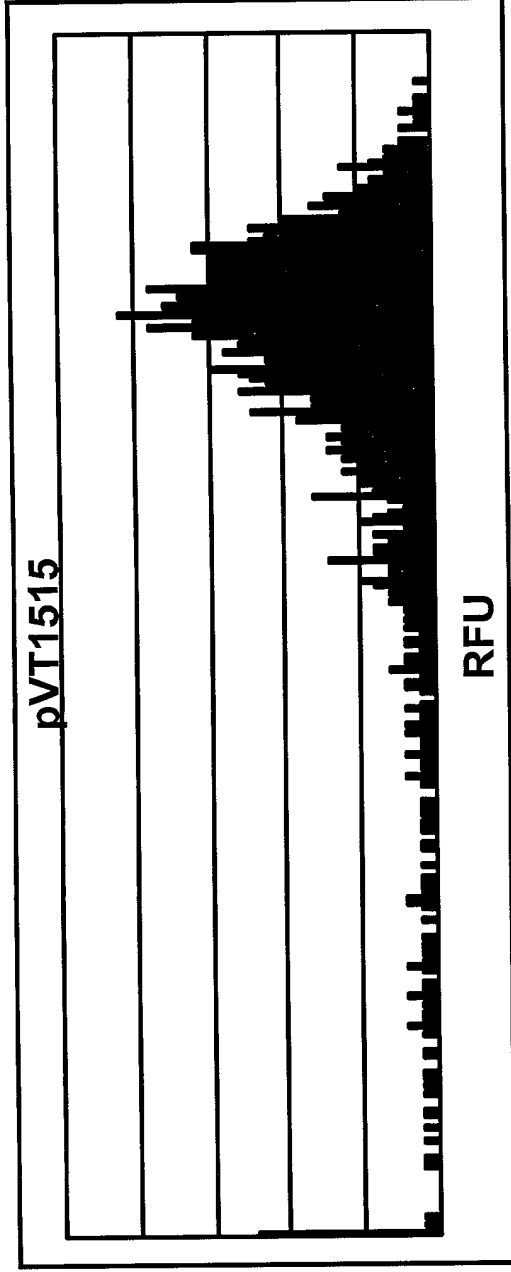


Figure 19

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Cad5CD/TCFDN

Cad5CD		TcfDN		Cad5CD		TcfDN		Clone ID	Accession No.	GeneName
Ratio		Ratio		z		z				
-2.2		-1.8		-7.3		-5.5		3580257	AP001708	genomic DNA, chromosome 21q
-1.5		-1.4		-5.5		-4.5		179196	AK025459	cDNA: highly similar to tra1 homologue of murine tumor rejection antigen gp96.
-1.9		-1.7		-5.4		-4.4		4291484	M55536	glucose transporter pseudogene.
-1.6		-1.3		-5.2		-3.7		1992945	AF016052	zinc finger protein ZNF191
-1.8		-1.5		-4.5		-3.3		23770	X57351	1-8D gene from interferon-inducible gene family.
-1.4		-1.7		-4.1		-6.8		459372	AF255303	membrane-associated nucleic acid binding protein
-1.3		-1.4		-3.8		-4.3		5188302	M26708	prothymosin alpha (ProT-alpha)
-1.5		-1.6		-3.7		-4.9		5046235	AAC72274	ZO-3
-1.3		-1.3		-3.6		-3.2		3592429	CAA26743	E1b 55k protein (transformation)
-1.6		-2		-3.5		-5.0		2834343	U52682	lymphocyte specific interferon regulatory factor 4 (LSIRF/IRF4)
-1.3		-1.4		-3.3		-4.5		2155121	X79535	beta tubulin
-1.3		-1.3		-3.3		-3.8		5003513	X54134	protein tyrosine phosphatase epsilon.
-1.4		-1.7		-3.3		-5.2		2833609	X05908	lipocortin.
-1.2		-1.2		-3.2		-3.0		2552381	M36981	putative NDP kinase (nm23-H2S)
-1.5		-1.6		-3.2		-3.3		2822027	AB002341	KIAA0343
1.3		1.3		3.2		3.4		4062068	AF107885	Ch 14q24.3, transforming growth factor-beta 3 (TGF-beta 3), unknown genes
1.3		1.4		3.4		3.6		4721478	AB003103	26S proteasome subunit p55
1.4		1.3		3.7		3.0		3865578	U86282	olfactory receptor (OR7-86) pseudogene

Figure 20

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Cad5CD

Ratio	Ratio	z	z	Clone ID	Accession No.	GeneName
-2.3	-1.4	-4.4	-1.8	5047895	AF177394	dickkopf-1 (DKK-1)
-2.2	-1.5	-4.2	-2.2	3050732	AF078165	axin-2
-1.4	-1.1	-3.7	-1.6	380006	M29064	hnRNP B1.
-1.3	-1.2	-3.5	-2.2	1511778	M73554	bcl-1 (cyclin D1)
-1.6	-1.5	-3.2	-2.7	2120743	AK023638	cDNA FLJ13576 fis.
-1.3	-1.2	-3.1	-2.9	4163444	M26697	nucleolar protein (B23)
-1.7	-1.6	-3.1	-2.6	1658215	X61118	TTG-2 cysteine rich protein with LIM motif.
-1.7	-1.4	-3.1	-2.0	1921238	M20681	glucose transporter-like protein-III (GLUT3)
-1.3	-1.1	-3.0	-1.4	2135733	AY007131	clone CDABP0045
-1.6	-1.4	-3.0	-2.3	4760384	AF155661	pyruvate dehydrogenase (PDH)
-1.6	-1.5	-3.4	-2.9	968676	S53354	B-cell activation protein=B-G antigen IgV domain homolog
1.3	1.1	3.1	1.0	5207613		Incyte EST
1.3	1.3	3.1	2.4	4879313	AP001676	genomic DNA, chromosome 21q
1.6	1.5	3.1	2.3	4271973	AF125348	caveolin 1 (CAV1)
1.4	1.2	4.1	2.4	2893021	AP001700	genomic DNA, chromosome 21q

Figure 21

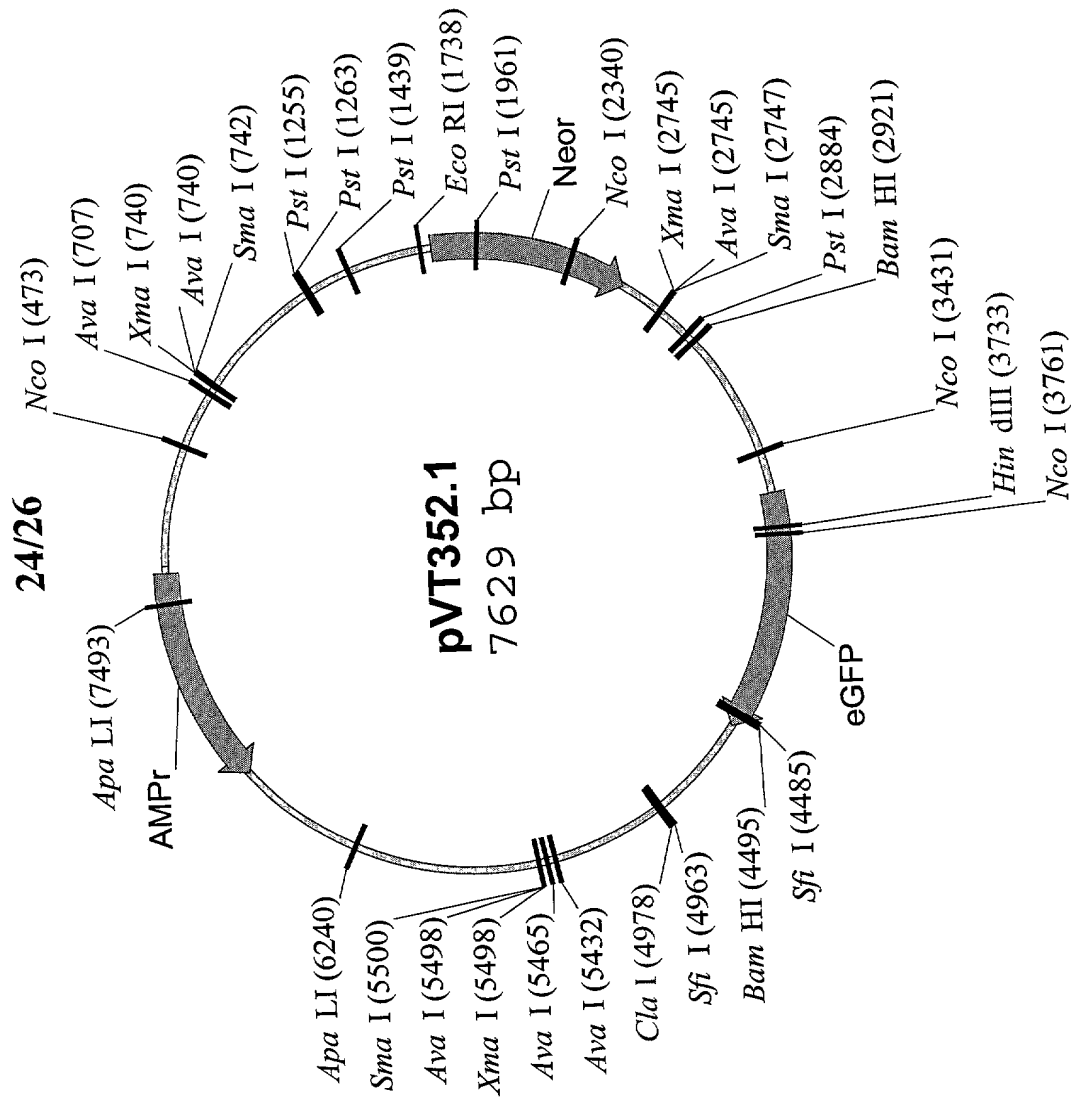


Figure 22

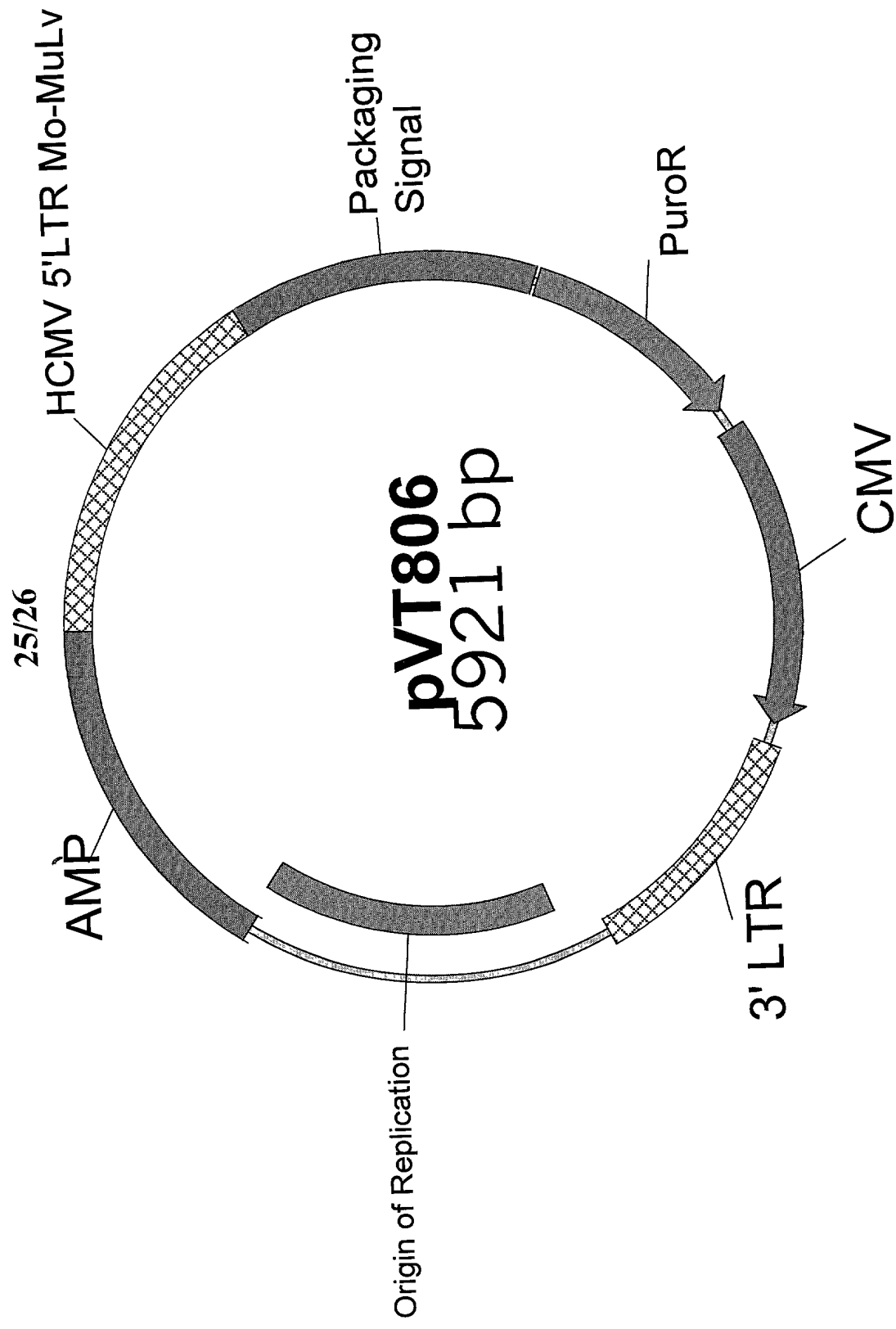


Figure 23

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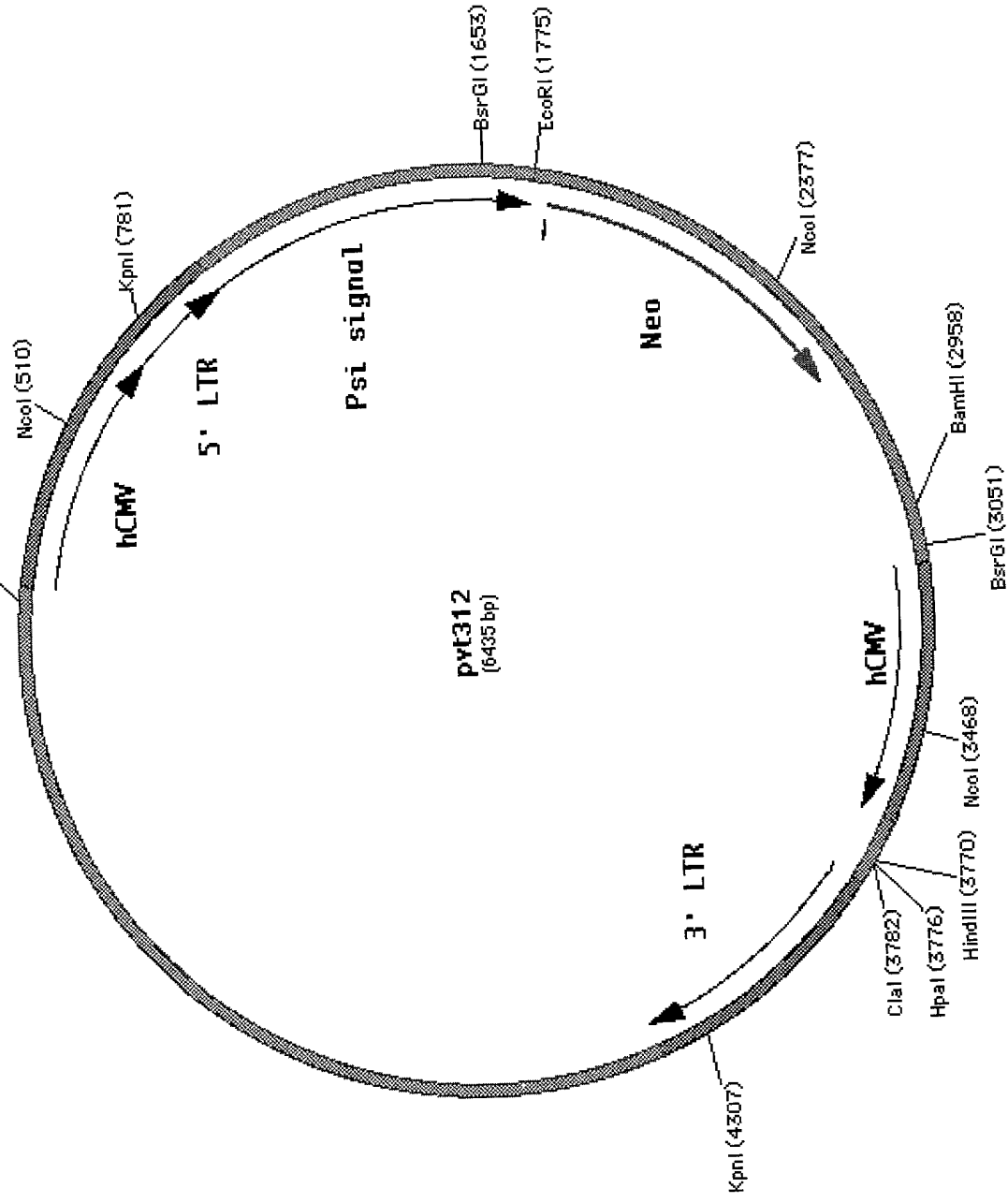


Figure 24